Program: *Phytophthora ramorum* Date: September 3, 2004

Trace forward and national surveys continue as PPQ determines the distribution of *P. ramorum.* There are no new positive locations for this week. As of September 2, 2004, the total number of confirmed positive locales from the trace forward, national, and other survey finds remains at 157 in 21 States. The total includes three residential finds; two in Georgia and one in South Carolina and one environs find in New York. The breakdown per State is: AL (3), AR(1), AZ (1), CA(53), CO(1), FL(6), GA(18), LA(5), MD(2), NC(9), NJ(1), NM(1), NY(1), OK(1), OR(10), PA(indoor), SC(3), TN(2), TX(11), VA(2) and WA (25).

APHIS - PPQ *P. ramorum* National Survey activities are complete in 13 States in the Western Region (AK, AR, AZ, CA, IA, ID, LA, MO, NE, ND, OK, SD, and MT); diagnostic results pending. As of September 2, 2004, participating States through out the nation have surveyed 2,166 sites and have collected 39,406 samples; 15 national survey sites are confirmed positive. The number of confirmed positives (15) is a downward adjustment due to a re-categorization of finds by Washington State. For more information on the PPQ *P. ramorum* National Survey, please refer to http://www.ceris.purdue.edu/napis/pests/sod/natplan/plan0403/index.html.

The US Forest Service *P. ramorum* detection surveys continue; all sampling results are either negative or still pending to date, with the exception of the 2 positive coast live oak trees in Golden Gate Park, San Francisco County, Ca., and 11 positives in the Regulated Area of Curry County, CA. As of September 3, 2004, the USFS has collected 2,430 samples from 610 nursery perimeter surveys in 32 States and 1,233 samples from 399 general forest surveys in 18 States. For more information on the Forest Service *P. ramorum* survey/ sampling methods, please refer to http://www.na.fs.fed.us/spfo/fhm/sod/sod_natnl.pdf.

The Joint Genome Institute (JGI) hosted a Phytophthora Genome Sequence Annotation Jamboree, August 15-20, 2004 at its Walnut Creek, California production sequencing facility. Forty genomics experts compared the genomes of *P. ramorum* and *P. sojae* (*P. sojae* causes over $1 billion annually in soybean damage). Better DNA fingerprinting of *P. ramorum* will provide for a more sensitive PCR- (Polymerase Chain Reaction) based diagnostic test. It was also confirmed that *P. ramorum* is not a new hybrid between two other species, as most genes do not occur in two copies.